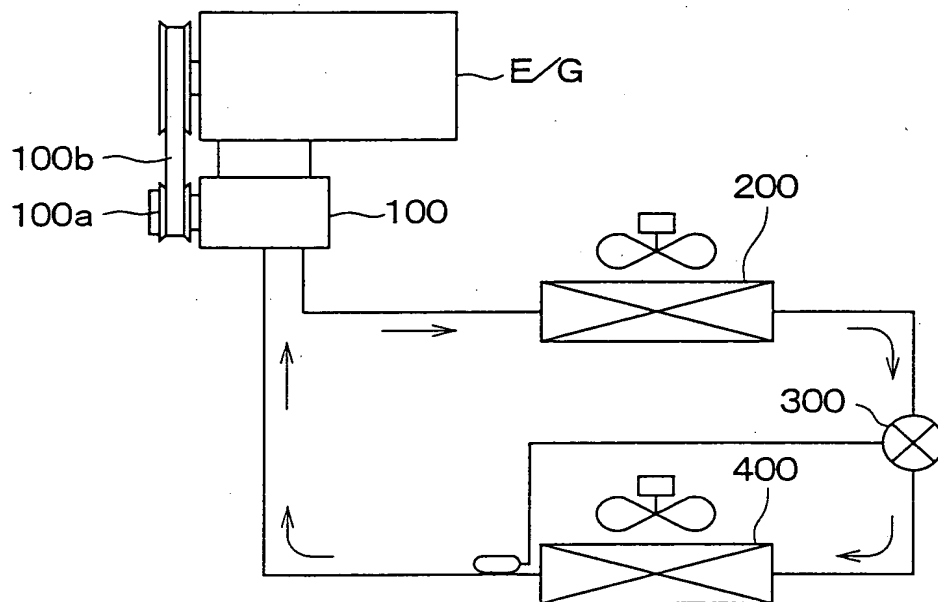


FIG. 1



1. *Phylogenetic relationships* among the studied taxa were determined using the maximum parsimony (MP) method. The MP analysis was performed using the program PAUP 4.0 (Felsenstein, 1999). The heuristic search was conducted using 1000 random starting trees. The tree was collapsed using the 95% bootstrap support (BS) value. The BS values were calculated using 1000 bootstrap replicates. The tree was rooted using the outgroup taxa. The tree was rooted using the outgroup taxa. The tree was rooted using the outgroup taxa.

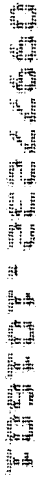


FIG. 3

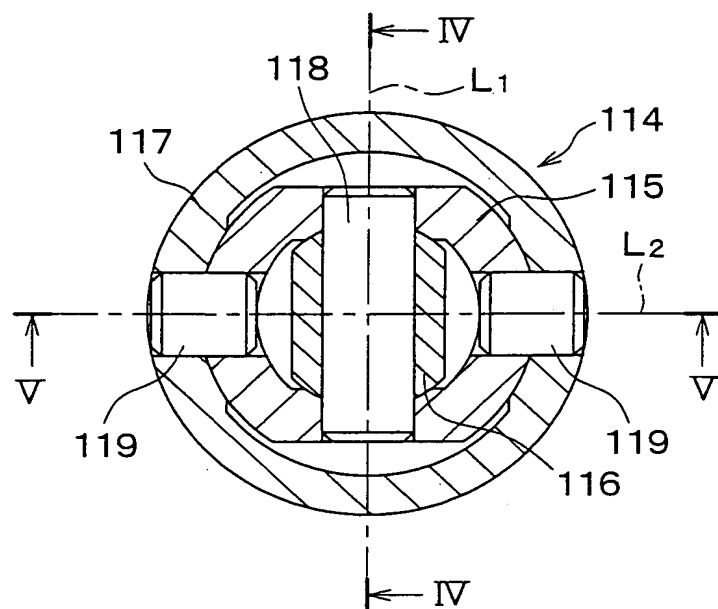


FIG. 4

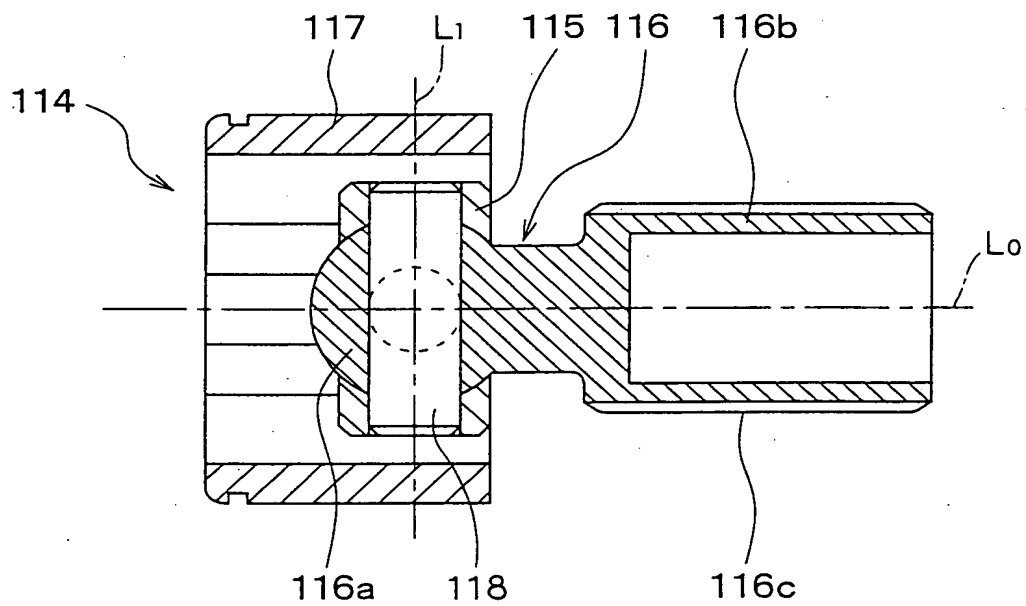


FIG. 5

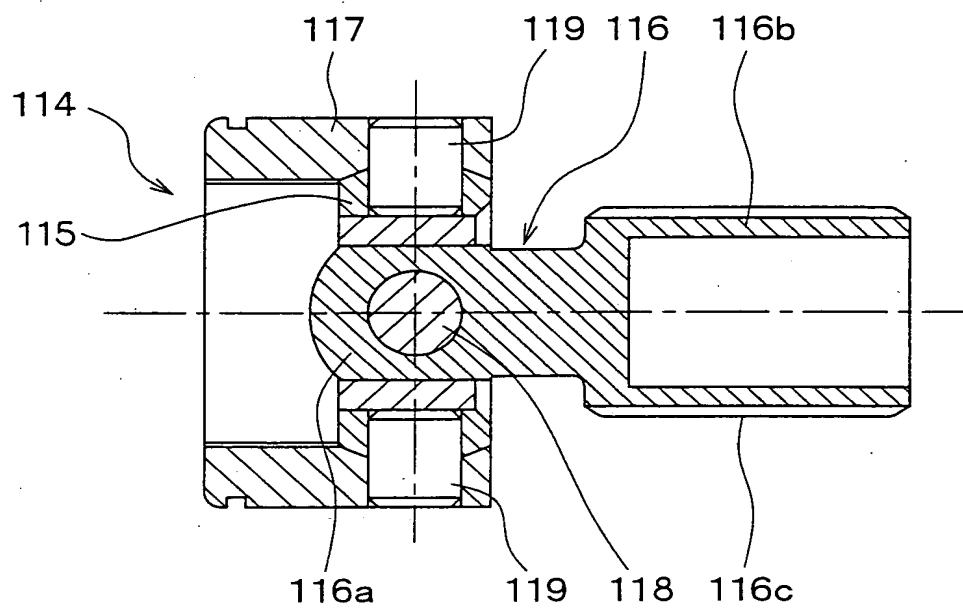


FIG. 6

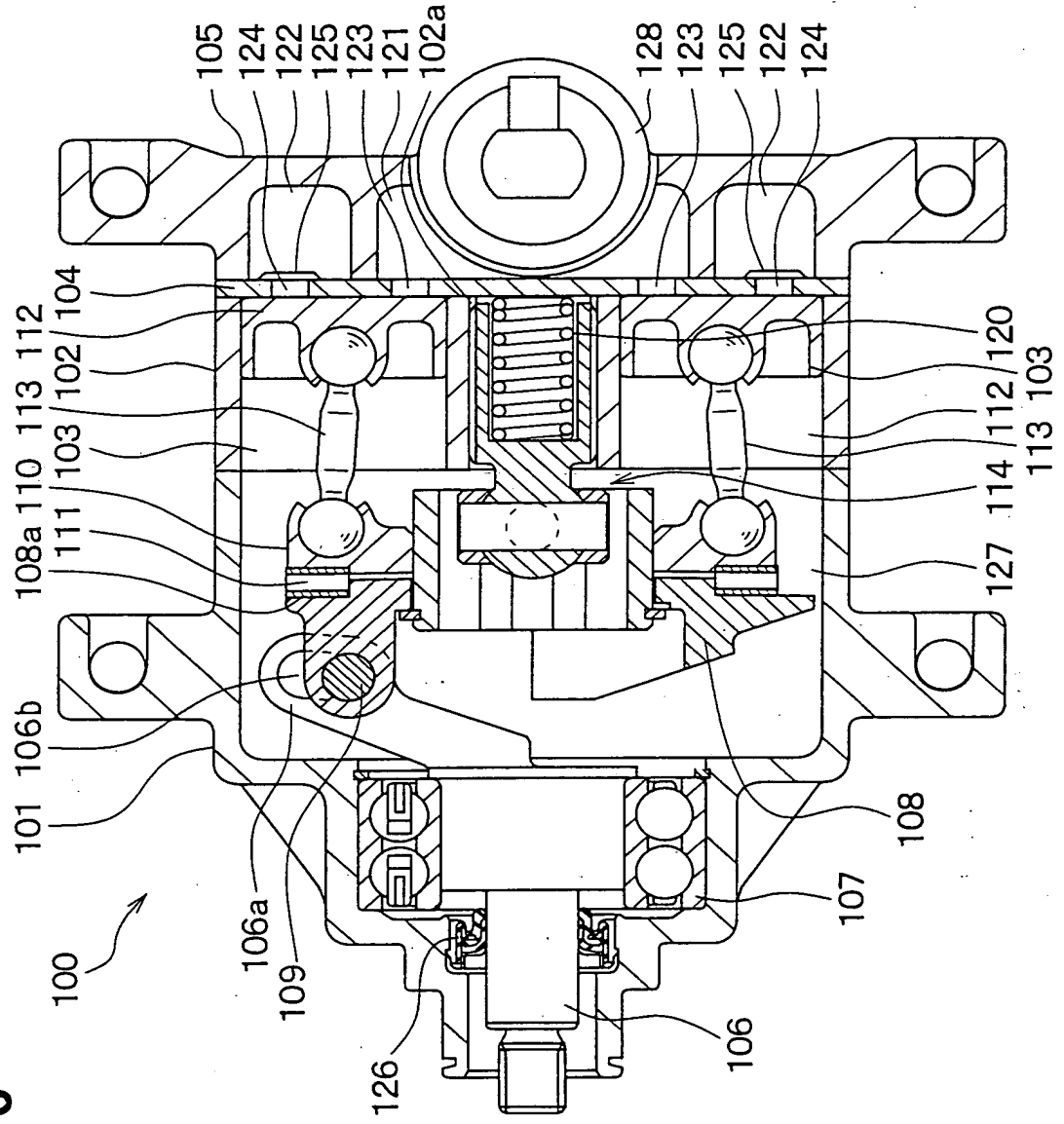


FIG. 7

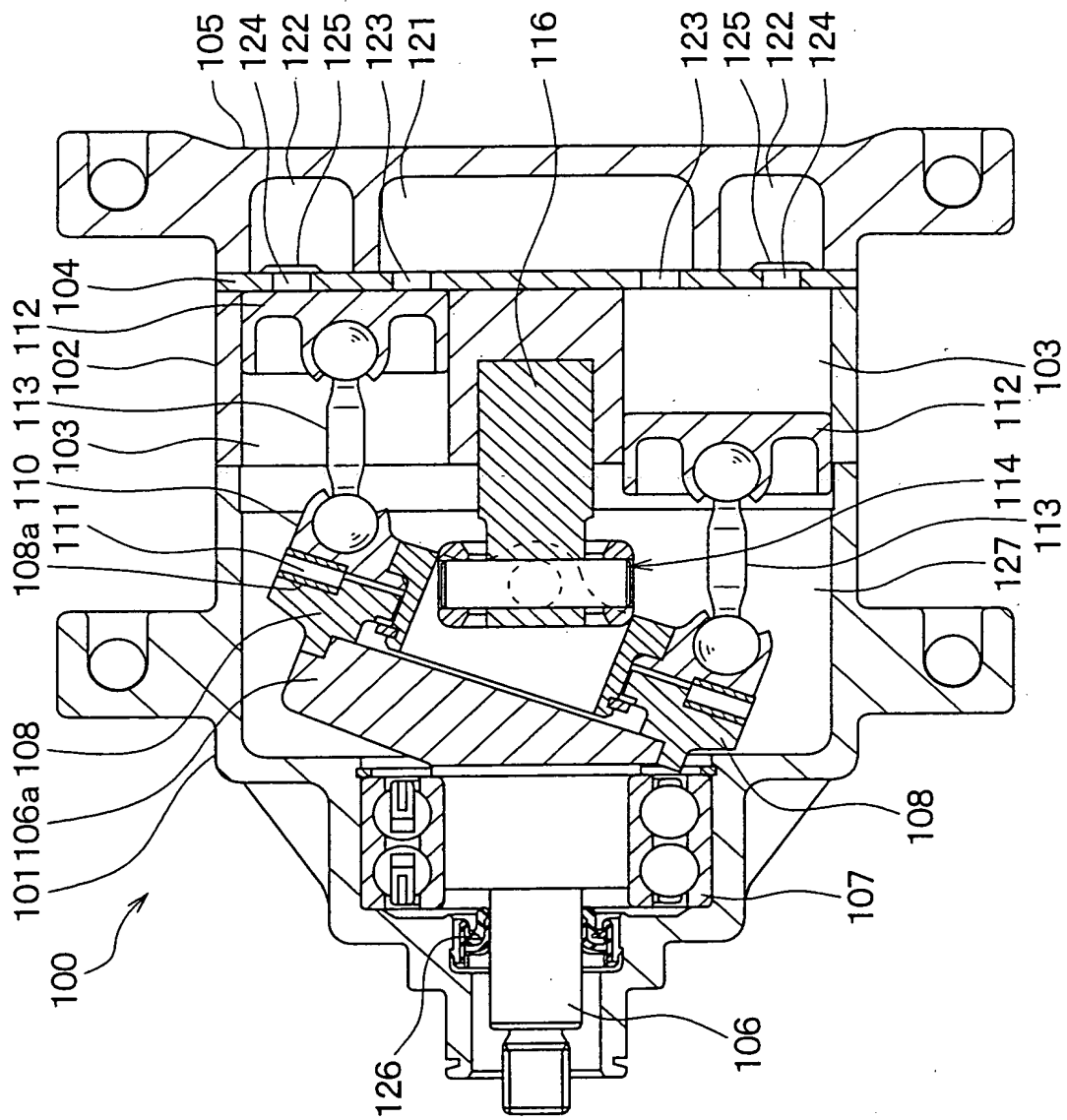


FIG. 8

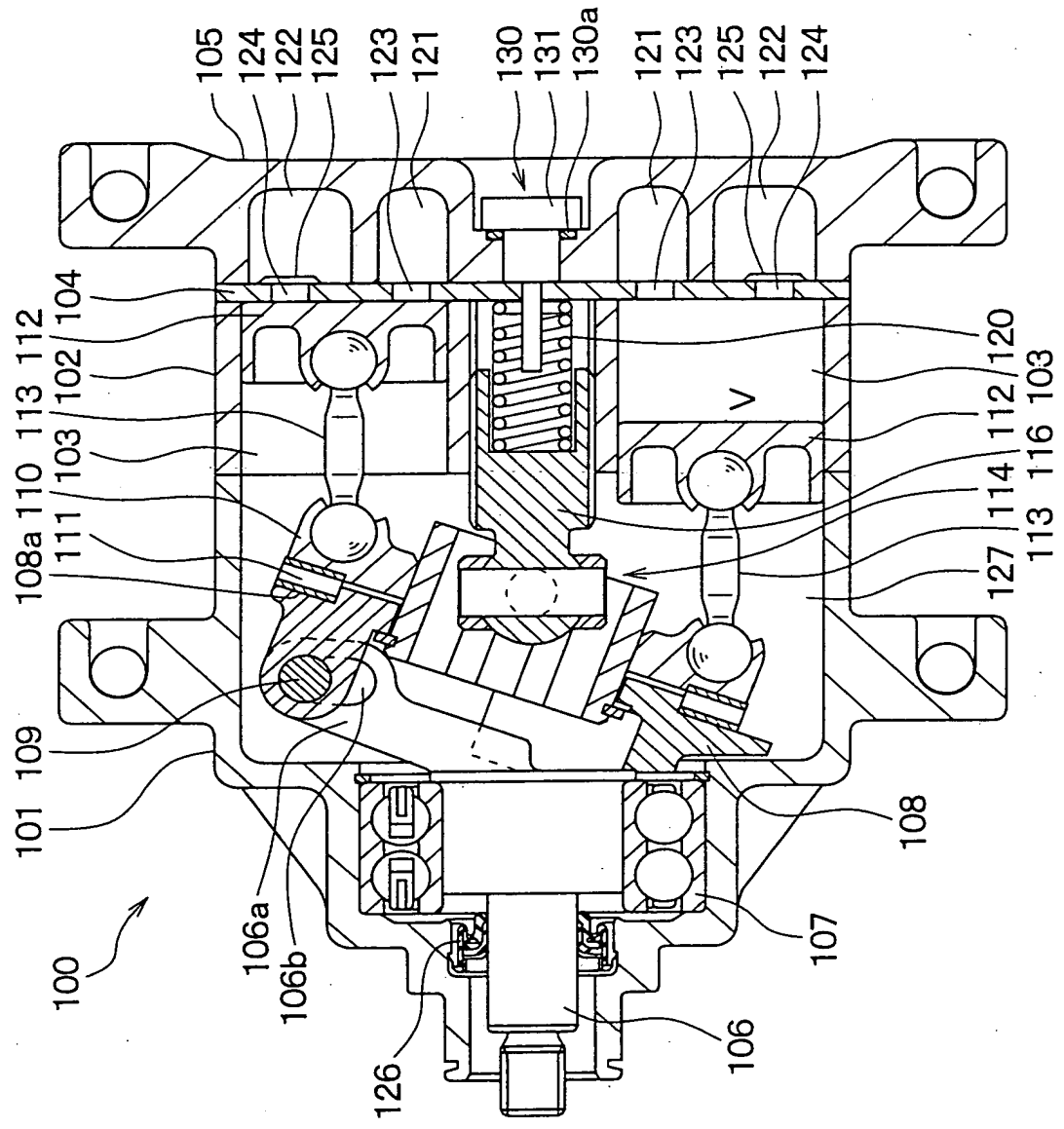


FIG. 9

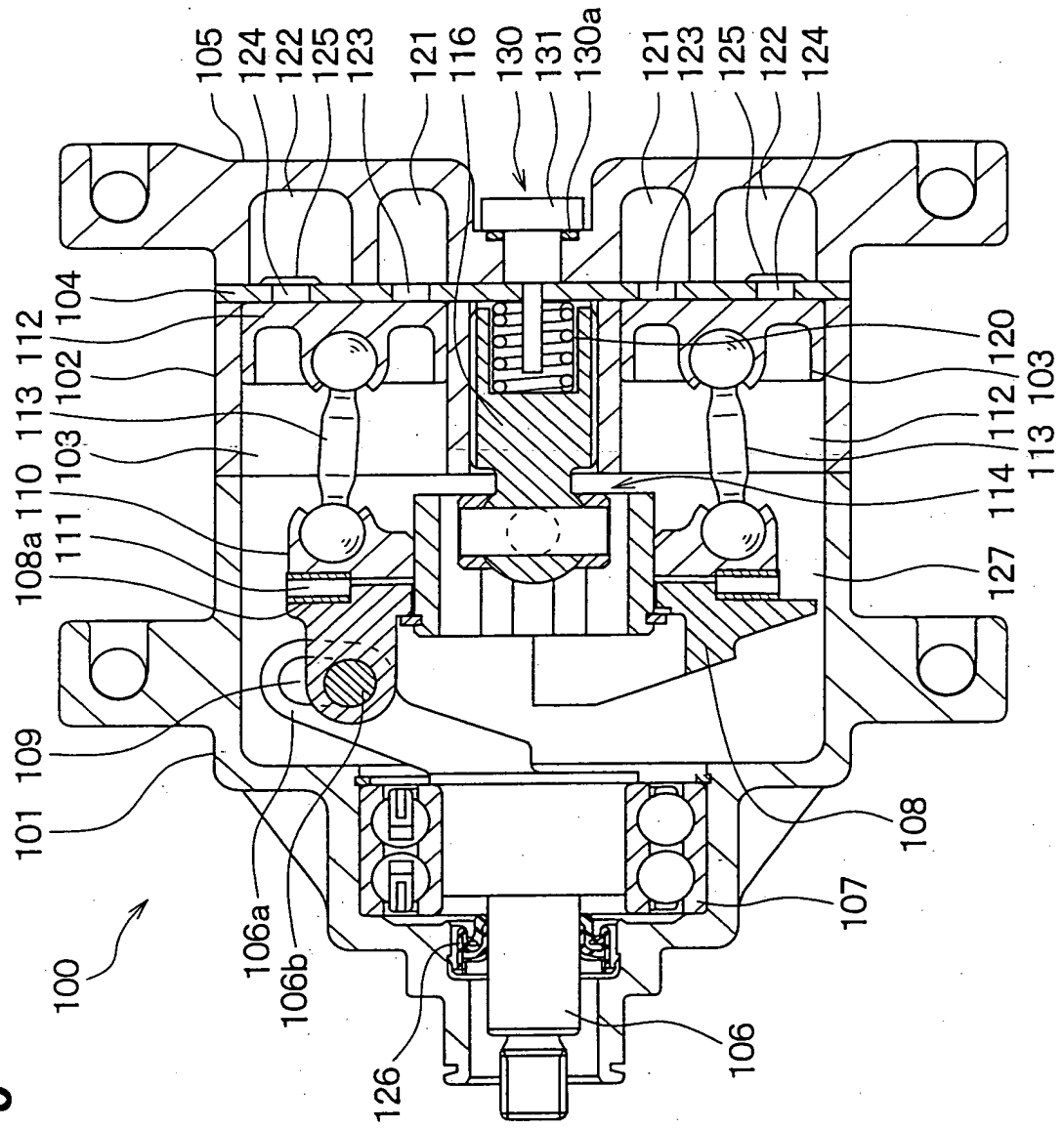


FIG. 10

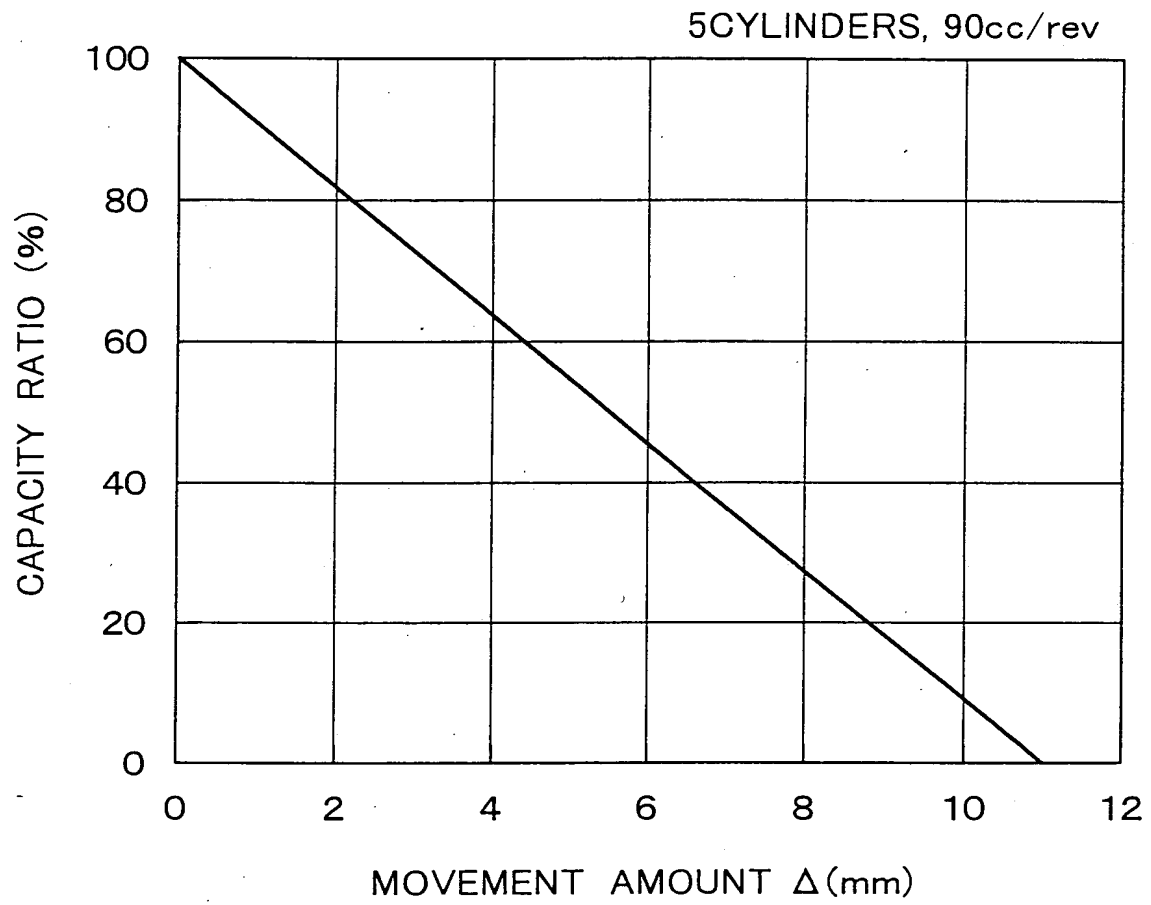


FIG. 11

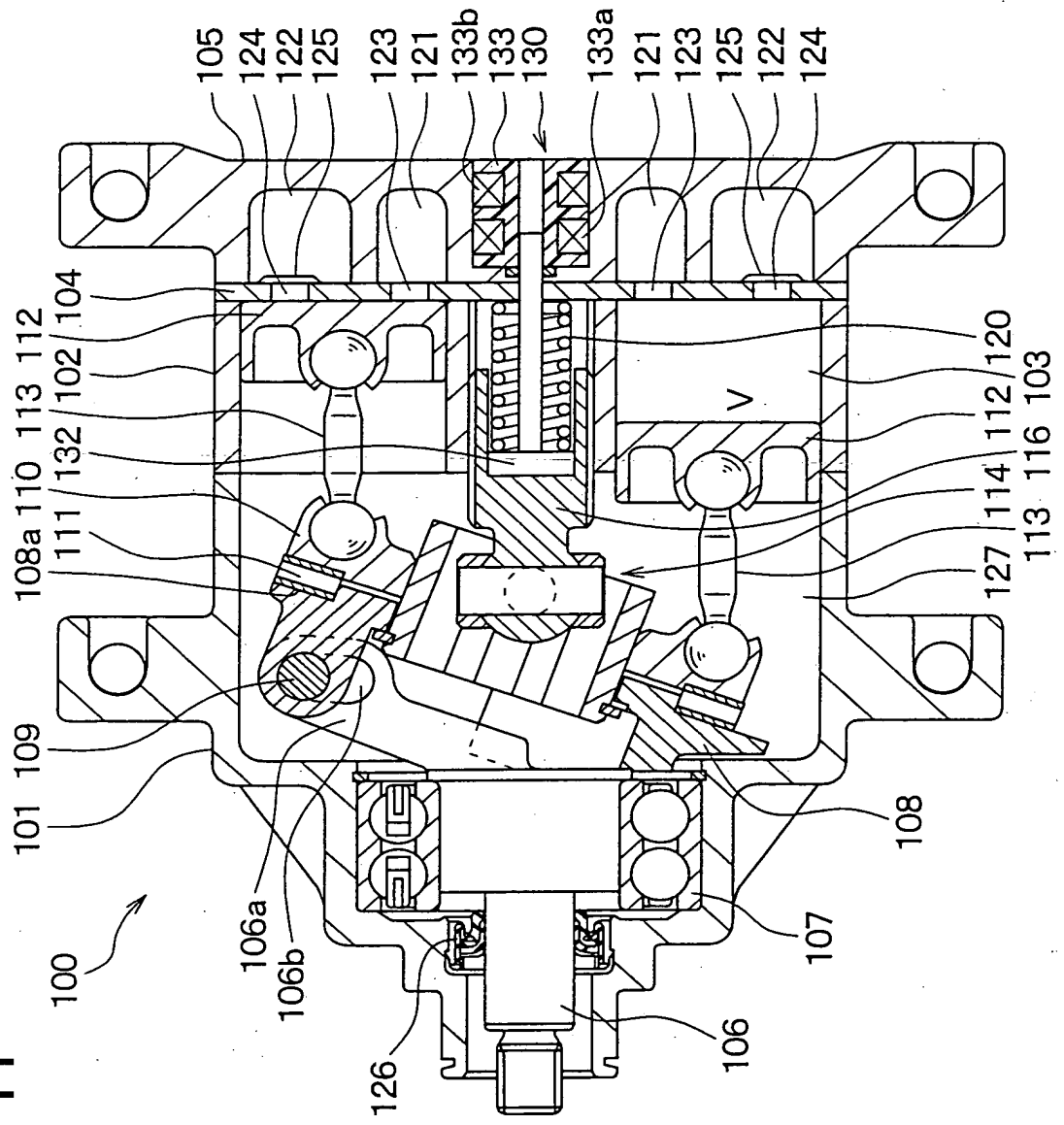


FIG. 12A

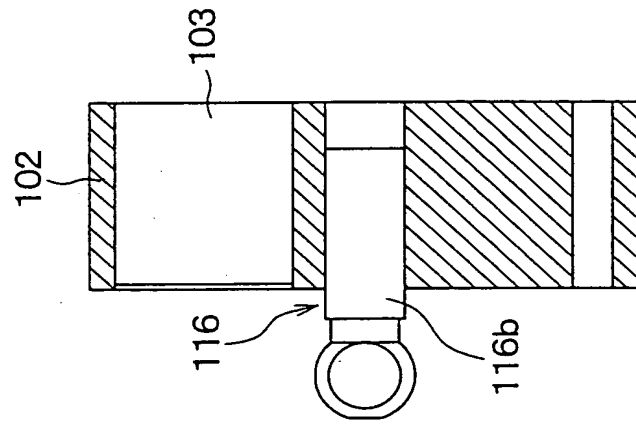


FIG. 12B

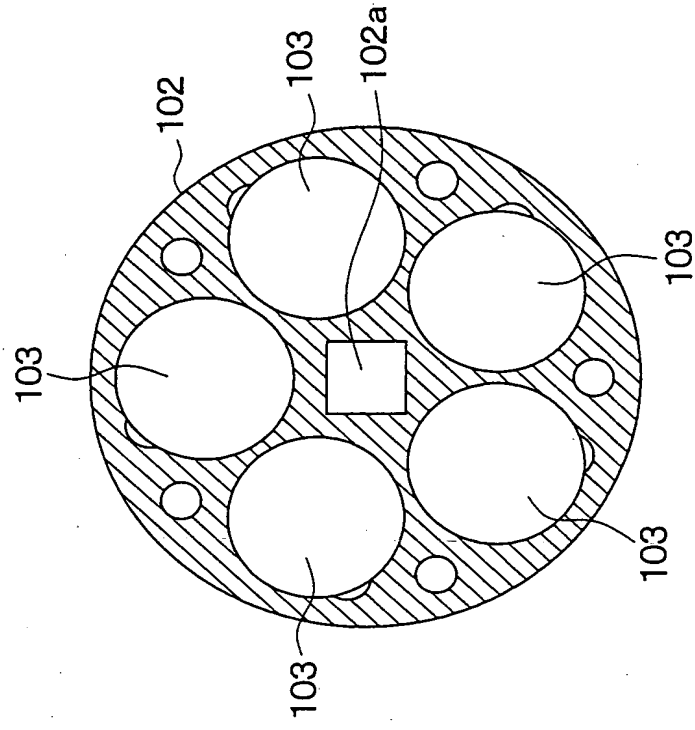


FIG. 13A

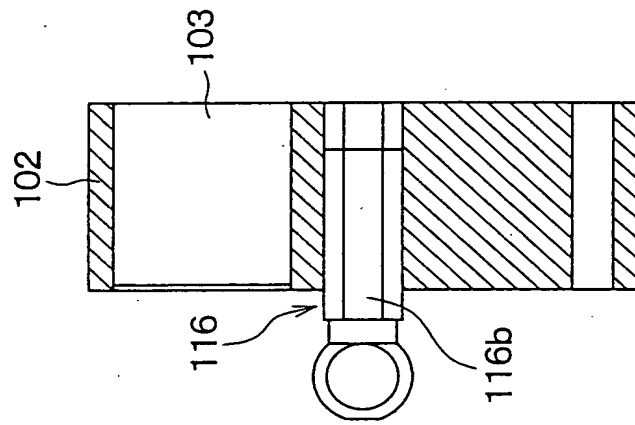


FIG. 13B

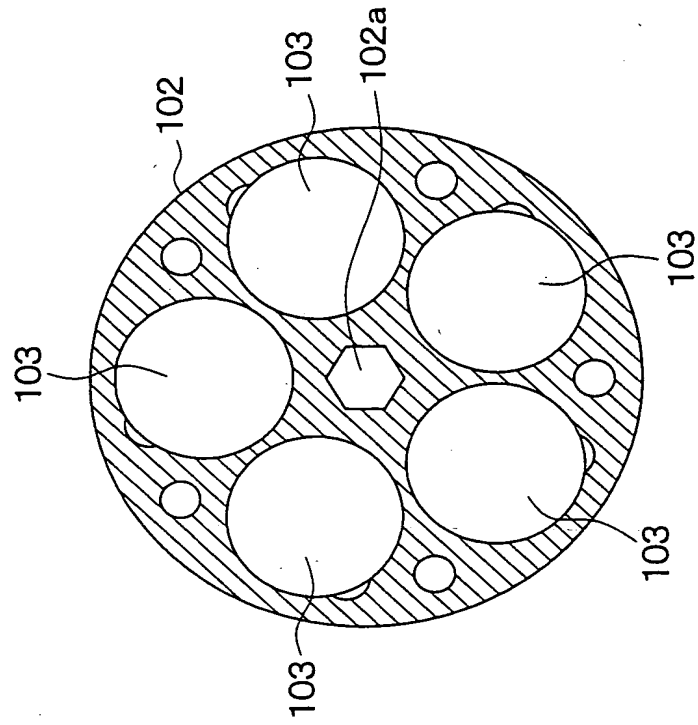


FIG. 14A

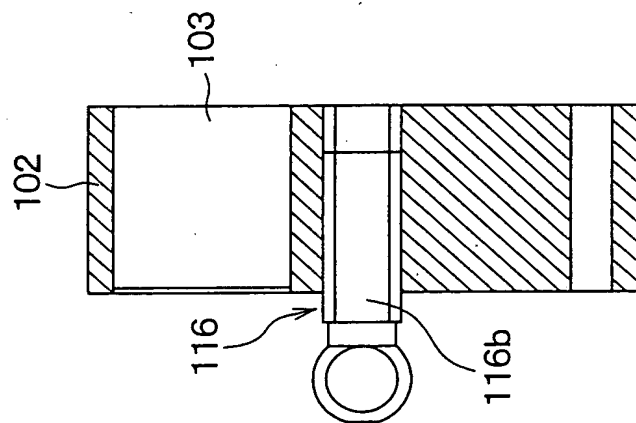
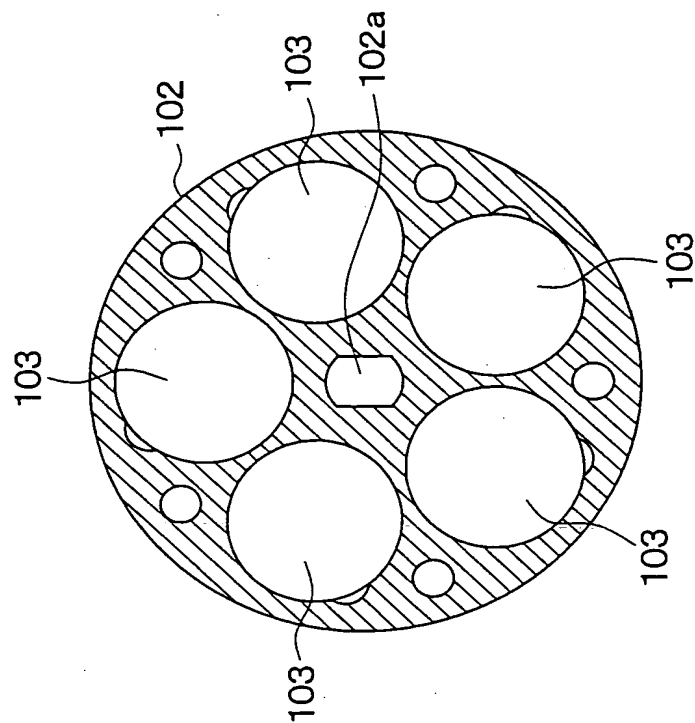


FIG. 14B



CO **CO**

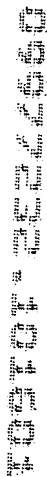


FIG. 16

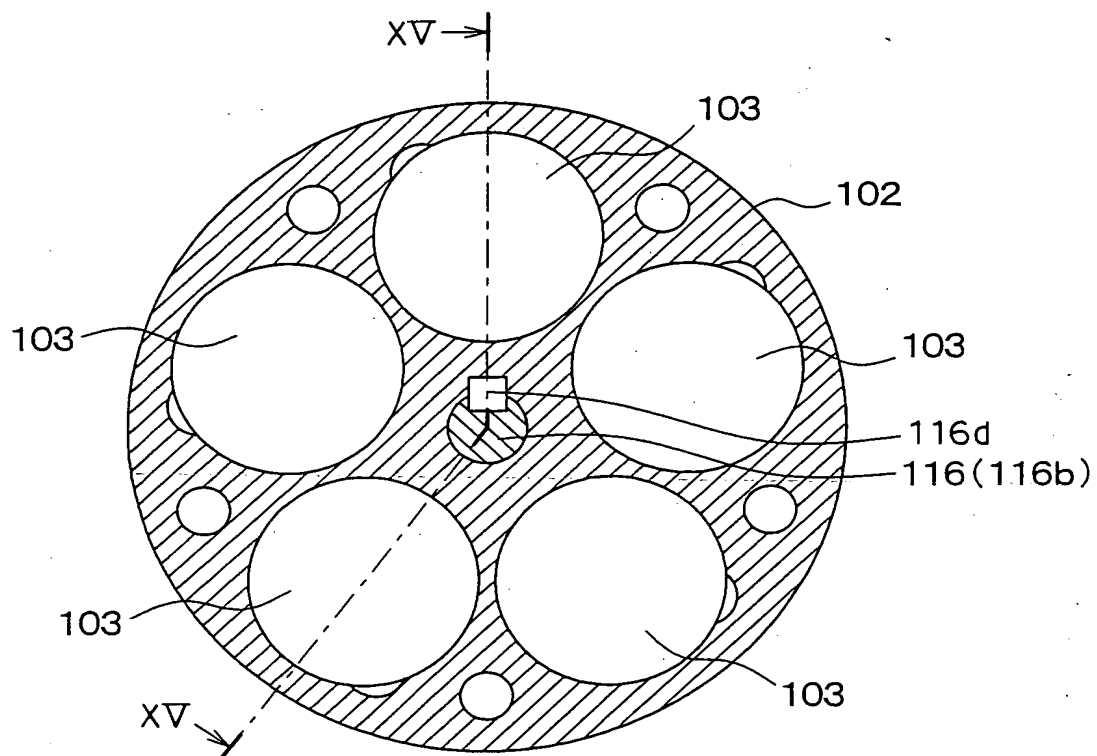


FIG. 17

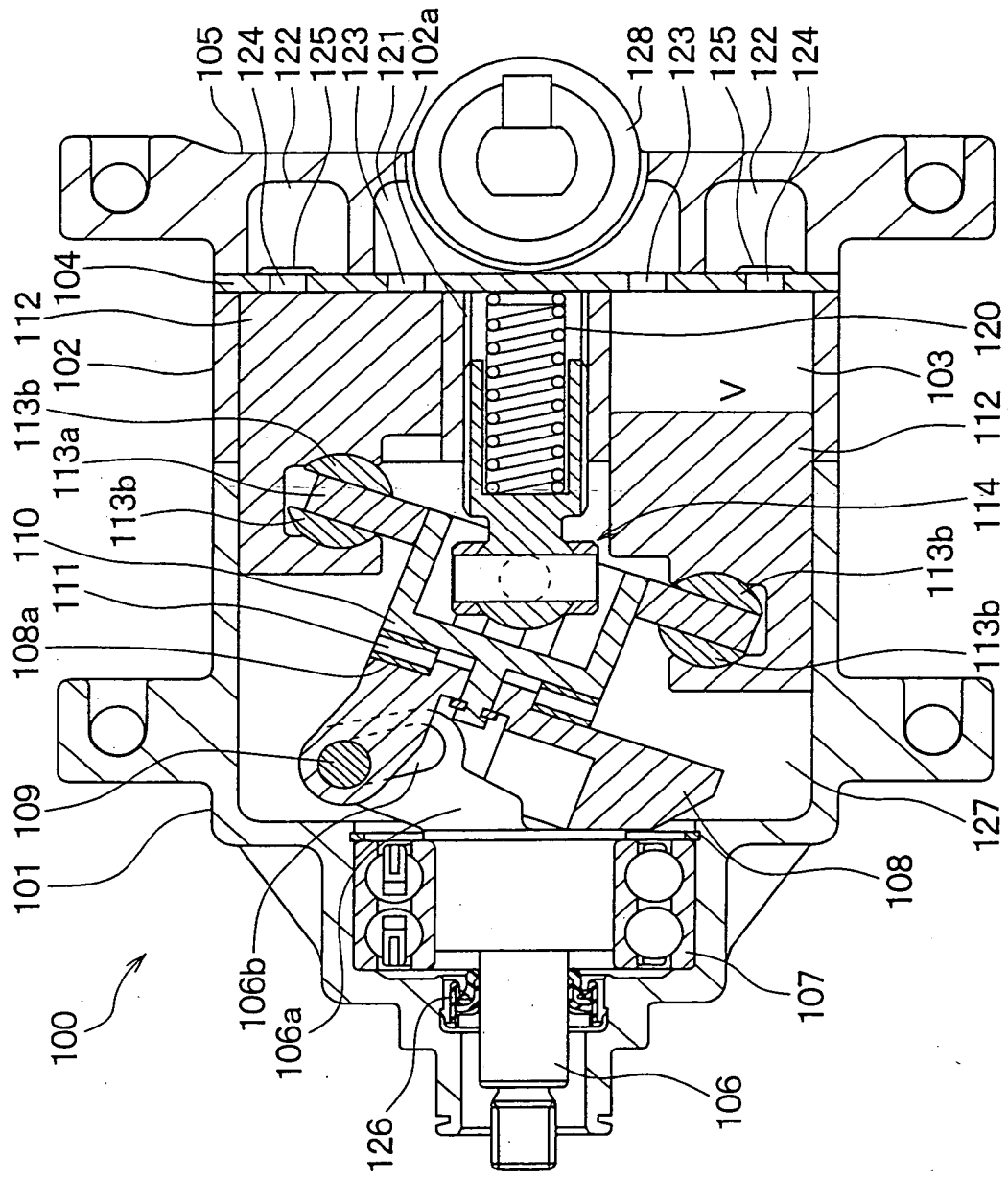


FIG. 18

